

# Sequence Scan SEQ ID No: 21+22

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	972	100.0	972	6	AX593579			AX593579 Sequence
	2	972	100.0	2229	6	AX593601			AX593601 Sequence
	3	349	35.9	939	6	AX593587			AX593587 Sequence
c	4	265.4	27.3	30176	8	SPAC186			AL157811 S.pombe c
	5	216.4	22.3	1423	1	BACLDHAA			M22305 B.megateriu
c	6	205.2	21.1	10029	1	AE006274			AE006274 Lactococc
	7	201.2	20.7	11158	1	AE007540			AE007540 Clostridi
c	8	200.6	20.6	301439	1	AE015943			AE015943 Clostridi
	9	199.4	20.5	948	1	AY098994			AY098994 Clostridi
	10	196.6	20.2	975	6	AR348221			AR348221 Sequence
c	11	196.2	20.2	302363	1	AE016948			AE016948 Enterococ

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	972	100.0	972	6	AAD41577			Aad41577 Kluyverom
	2	972	100.0	2229	6	AAD41597			Aad41597 Promoter-
	3	349	35.9	939	6	AAD41584			Aad41584 Torulaspo
	4	234	24.1	924	13	ADS48457			Ads48457 Bacterial
	5	216.4	22.3	957	9	ACF35756			Acf35756 B. megate
c	6	205.2	21.1	110000	6	ABA90521_03			Continuation (4 of
	7	204	21.0	945	13	ADT43579			Adt43579 Bacterial
	8	196.6	20.2	975	10	ADC93205			Adc93205 E. faeciu
	9	192.6	19.8	936	13	ADT41727			Adt41727 Bacterial
	10	191.4	19.7	957	10	ADH83127			Adh83127 Enterococ

Database : Issued Patents\_NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	196.6	20.2	975	4	US-09-107-532A-2832	Sequence 2832, Ap
2	191.4	19.7	957	4	US-09-134-000C-1012	Sequence 1012, Ap
3	183.8	18.9	969	4	US-09-710-279-1411	Sequence 1411, Ap
4	183.8	18.9	969	4	US-09-710-279-2383	Sequence 2383, Ap
5	183.8	18.9	993	3	US-09-134-001C-1491	Sequence 1491, Ap
c 6	183.8	18.9	3019	4	US-09-710-279-4355	Sequence 4355, Ap
7	183.8	18.9	4093	4	US-09-710-279-3793	Sequence 3793, Ap
8	172.6	17.8	3264	4	US-08-956-171E-424	Sequence 424, App
9	172.6	17.8	3264	4	US-08-781-986A-424	Sequence 424, App
c 10	159.8	16.4	14333	4	US-08-956-171E-57	Sequence 57, Appl
c 11	159.8	16.4	14333	4	US-08-781-986A-57	Sequence 57, Appl
12	158.2	16.3	924	4	US-09-107-532A-620	Sequence 620, App
13	155.2	16.0	999	4	US-09-583-110-1930	Sequence 1930, Ap
14	153.8	15.8	995	4	US-09-107-433-2149	Sequence 2149, Ap
c 15	153.6	15.8	5278	3	US-08-961-527-227	Sequence 227, App
c 16	147.2	15.1	5449	3	US-09-546-990-1	Sequence 1, Appli

Database :           Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	972	100.0	972	10	US-09-992-430B-21		Sequence 21, Appl
2	972	100.0	2229	10	US-09-992-430B-43		Sequence 43, Appl
3	349	35.9	939	10	US-09-992-430B-29		Sequence 29, Appl
4	234	24.1	924	17	US-10-369-493-26887		Sequence 26887, A
5	216.4	22.3	957	16	US-10-154-460-45		Sequence 45, Appl
6	204	21.0	945	17	US-10-369-493-42017		Sequence 42017, A
7	192.6	19.8	936	17	US-10-369-493-40165		Sequence 40165, A
8	186.2	19.2	28690	9	US-09-070-927A-138		Sequence 138, App
9	183.6	18.9	1255	9	US-09-971-361-2		Sequence 2, Appli

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est2:\*  
 3: gb\_htc:\*  
 4: gb\_est3:\*  
 5: gb\_est4:\*  
 6: gb\_est5:\*  
 7: gb\_est6:\*  
 8: gb\_gss1:\*  
 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	152	15.6	968	9	CNS06Y1R			AL420469 T3 end of
	2	144.4	14.9	1227	3	CR725013			CR725013 Tetraodon
	3	144.4	14.9	1277	3	CR726668			CR726668 Tetraodon
	4	144.4	14.9	1279	3	CR727091			CR727091 Tetraodon
	5	142.8	14.7	1993	3	CR685436			CR685436 Tetraodon
	6	142.2	14.6	967	7	CK271702			CK271702 EST717780
	7	140.6	14.5	871	7	CK247148			CK247148 EST730785
	8	138.4	14.2	936	7	CK403761			CK403761 AUF_IfHdk
	9	138	14.2	949	7	CK870287			CK870287 AGENCOURT
	10	137.2	14.1	932	7	CF225147			CF225147 AGENCOURT
c	11	136.2	14.0	889	5	BU714716			BU714716 SJMBPB10
	12	135	13.9	936	5	BQ963532			BQ963532 AGENCOURT
	13	134.8	13.9	882	7	CR432844			CR432844 CR432844
	14	134.8	13.9	898	5	BX714742			BX714742 BX714742

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1614.5	99.4	324	5	AAE25510	Aae25510 Kluyverom
2	952.5	58.6	313	5	AAE25511	Aae25511 Torulaspo
3	830	51.1	308	8	ADN20547	Adn20547 Bacterial
4	723.5	44.5	318	6	ABR82282	Abr82282 B. megate
5	694	42.7	318	8	ADN26369	Adn26369 Bacterial
6	689	42.4	312	8	ADS27445	Ads27445 Bacterial
7	687.5	42.3	319	8	ADN20416	Adn20416 Bacterial
8	663	40.8	312	8	ADS27646	Ads27646 Bacterial
9	663	40.8	319	5	AAE23265	Aae23265 Bacillus
10	654	40.2	319	2	AAR10591	Aar10591 L-lactic
11	649	39.9	310	8	ADS28441	Ads28441 Bacterial
12	646.5	39.8	317	6	ABM72014	Abm72014 Staphyloc
13	639	39.3	321	8	ADO59775	Ado59775 B. subtil
14	639	39.3	321	8	ADS44643	Ads44643 Bacterial
15	635	39.1	322	4	AAG82159	Aag82159 S. epider

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	648	39.9	317	1	US-08-748-068-3	Sequence 3, Appli
2	635	39.1	322	4	US-09-710-279-1412	Sequence 1412, Ap
3	635	39.1	322	4	US-09-710-279-2384	Sequence 2384, Ap
4	635	39.1	330	3	US-09-134-001C-4328	Sequence 4328, Ap
5	599	36.9	324	4	US-09-107-532A-6486	Sequence 6486, Ap
6	585	36.0	318	4	US-09-134-000C-4417	Sequence 4417, Ap
7	578	35.6	331	4	US-09-711-681-4	Sequence 4, Appli
8	578	35.6	331	4	US-10-274-266-4	Sequence 4, Appli
9	576.5	35.5	331	4	US-09-107-433-4752	Sequence 4752, Ap
10	576.5	35.5	332	4	US-09-583-110-4591	Sequence 4591, Ap
11	576	35.4	351	4	US-09-949-016-11252	Sequence 11252, A
12	576	35.4	351	4	US-09-949-016-11253	Sequence 11253, A
13	569.5	35.0	307	4	US-09-107-532A-4274	Sequence 4274, Ap
14	562.5	34.6	327	1	US-08-748-068-2	Sequence 2, Appli

Database :           Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1625	100.0	323	10	US-09-992-430B-22	Sequence 22, Appl
2	952.5	58.6	313	10	US-09-992-430B-30	Sequence 30, Appl
3	830	51.1	308	15	US-10-369-493-3200	Sequence 3200, Ap
4	723.5	44.5	318	14	US-10-154-460-46	Sequence 46, Appl
5	694	42.7	318	15	US-10-369-493-9022	Sequence 9022, Ap
6	689	42.4	312	15	US-10-369-493-16478	Sequence 16478, A
7	687.5	42.3	319	15	US-10-369-493-3069	Sequence 3069, Ap
8	663	40.8	312	15	US-10-369-493-16679	Sequence 16679, A



Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	838	51.6	330	2	T50135	probable l-lactate
2	733	45.1	313	2	E96932	L-lactate dehydrog
3	723.5	44.5	318	1	DEBSLM	L-lactate dehydrog
4	687.5	42.3	319	2	S36863	L-lactate dehydrog
5	679	41.8	318	2	S08182	L-lactate dehydrog
6	673	41.4	319	2	S08183	L-lactate dehydrog
7	669	41.2	317	2	S00019	L-lactate dehydrog
8	667.5	41.1	317	2	T44580	lactate dehydrogen
9	659	40.6	317	2	B29704	L-lactate dehydrog
10	649	39.9	310	2	A84142	L-lactate dehydrog
11	648	39.9	317	1	DEBSLF	L-lactate dehydrog
12	647.5	39.8	317	2	D89787	L-lactate dehydrog
13	639.5	39.4	326	1	DELBLA	L-lactate dehydrog
14	639	39.3	321	2	E69649	L-lactate dehydrog
15	627	38.6	314	2	H86671	L-lactate dehydrog
16	617	38.0	313	2	AC1101	L-lactate dehydrog
17	617	38.0	313	2	AC1463	L-lactate dehydrog
18	613	37.7	310	1	JX0090	L-lactate dehydrog

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	843	51.9	324	2	Q7SES6	Q7ses6 neurospora
2	838	51.6	330	1	LDH_SCHPO	Q9p7p7 schizosacch
3	753	46.3	315	1	LDH_CLOTM	Q8kqc4 clostridium
4	746	45.9	316	1	LDH_CLOTE	Q892u0 clostridium
5	733	45.1	313	1	LDH1_CLOAB	Q97md1 clostridium
6	723.5	44.5	318	1	LDH_BACME	P00345 bacillus me
7	722	44.4	317	1	LDH_CLOPE	Q8xp62 clostridium
8	690	42.5	314	1	LDH1_BACAN	Q8lrw4 bacillus an
9	690	42.5	314	1	LDH1_BACC1	P62047 bacillus ce
10	690	42.5	314	2	Q63CN1	Q63cn1 bacillus ce
11	690	42.5	314	2	Q6HK31	Q6hk31 bacillus th
12	689	42.4	314	1	LDH1_BACCR	Q8lep4 bacillus ce
13	687.5	42.3	319	1	LDH_THEMA	P16115 thermotoga
14	679	41.8	311	1	LDH_THESA	Q7x5c9 thermoanaer
15	679	41.8	318	1	LDHP_BACPS	P14561 bacillus ps
16	673	41.4	319	1	LDHX_BACPS	P20619 bacillus ps
17	667.5	41.1	317	2	Q9S0N0	Q9s0n0 bacillus st
18	667	41.0	314	1	LDH2_BACAN	Q81k80 bacillus an
19	667	41.0	314	2	Q632G8	Q632g8 bacillus ce
20	667	41.0	314	2	Q6HC14	Q6hc14 bacillus th
21	667	41.0	317	1	LDH_BACCA	P10655 bacillus ca
22	665	40.9	314	1	LDH2_BACC1	P62048 bacillus ce
23	665	40.9	314	1	LDH2_BACCR	Q816g3 bacillus ce
24	659	40.6	317	1	LDH_BACCL	Q59244 bacillus ca